#6

SEQUENCE LISTING

<110> Wolfrain, Lawrence A
Letterio, John J

<120> FUNCTIONALIZED TGF-BETA FUSION PROTEINS

<130> 4239-61302

<140> US 10/017,372
<141> 2001-10-19

<150> US 60/242,292
<151> 2000-10-20

<160> 39

<170> PatentIn version 3.1

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<400> 6
cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg 45

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<220>
<223> Synthetic oligopeptide

a1 Cont

<400> 7

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 8
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<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
<221> CDS
<222> (1)..(1197)
<223>

<220>
<221> misc_feature
<222> (278)..(279)

<223> Maturation cleavage site

<400> 8

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atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg        48
Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1               5                   10                  15

tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc        96
Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
            20                  25                  30

tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc       144
Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45

att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc       192
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50                  55                  60

cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt       240
Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65                  70                  75                  80

tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag       288
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
                85                  90                  95

ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta       336
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
            100                 105                 110

atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc       384
Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
        115                 120                 125

cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg       432
His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
    130                 135                 140

ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc       480
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145                 150                 155                 160

aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat       528
Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
                165                 170                 175

gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca       576
Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
            180                 185                 190

ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg       624
Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
        195                 200                 205

acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc       672
Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
    210                 215                 220

tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat       720
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Cl' Cont

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Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225                 230                 235                 240

tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc      768
Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
                245                 250                 255

ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac      816
Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
            260                 265                 270

agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg      864
Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
        275                 280                 285

gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg      912
Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
    290                 295                 300

cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat      960
Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305                 310                 315                 320

gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac     1008
Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
                325                 330                 335

atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac     1056
Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
            340                 345                 350

cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg     1104
Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
        355                 360                 365

ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg     1152
Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
    370                 375                 380

gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga         1197
Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385                 390                 395
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a' cont

<210> 9
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<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
<221> misc_feature
<222> (278)..(279)
<223> Maturation cleavage site

<400> 9

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1               5                   10                  15
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

a' cont

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
275 280 285

Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385 390 395

<210> 10
<211> 362
<212> DNA
<213> Artificial Sequence

a' cont

<220>
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aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120

attcatgaac ccaagggctc catgccaatt tctgcctggg gccctgtccc tacatctgga 180

gcctagacac tcagtacagc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt 240

cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg 300

gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct 360

ga 362

<210> 11
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<212> PRT
<213> Artificial Sequence

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<220>
<221> PEPTIDE
<222> (1)..(8)
<223> FLAG tag

<400> 11

Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe
1 5 10 15

Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

a' Cont.

Ile Val Arg Ser Cys Lys Cys Ser
115 120

<210> 12
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
<221> CDS
<222> (1)..(1197)
<223>

<220>
<221> misc_feature
<222> (278)..(279)
<223> Maturation cleavage site

<400> 12

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1               5                   10                  15

tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc        96
Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
            20                  25                  30

tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc       144
Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45

att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc       192
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50                  55                  60

cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt       240
Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65                  70                  75                  80

tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag       288
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
                85                  90                  95

ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta       336
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
            100                 105                 110

atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc       384
Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
        115                 120                 125

cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg       432
His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
    130                 135                 140

ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc       480
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145                 150                 155                 160

aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat       528
Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
                165                 170                 175

gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca       576
Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
            180                 185                 190

ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg       624
Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
        195                 200                 205

acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc       672
```

a' cont.

```
Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
    210                 215                 220

tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat      720
Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225                 230                 235                 240

tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc      768
Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
                245                 250                 255

ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac      816
Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
            260                 265                 270

agc tcc cgg cac cgc cga gcc ctg gat acc aac tac tgc ttc agc tcc      864
Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
        275                 280                 285

acg gac tac aag gat gac gac gac aag gag aag aac tgc tgc gtg cgg      912
Thr Asp Tyr Lys Asp Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg
    290                 295                 300

cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat      960
Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305                 310                 315                 320

gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac     1008
Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
                325                 330                 335

atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac     1056
Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
            340                 345                 350

cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg     1104
Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
        355                 360                 365

ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg     1152
Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
    370                 375                 380

gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga         1197
Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385                 390                 395
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a' cont.

<210> 13
<211> 398
<212> PRT
<213> Artificial Sequence

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<223> Fusion oligonucleotide

<220>
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<222> (278)..(279)
<223> Maturation cleavage site

<400> 13

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            20                  25                  30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50                  55                  60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65                  70                  75                  80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
                85                  90                  95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
            100                 105                 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
        115                 120                 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
    130                 135                 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145                 150                 155                 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
                165                 170                 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
            180                 185                 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
        195                 200                 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
    210                 215                 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225                 230                 235                 240
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a' cont.

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
275 280 285

Thr Asp Tyr Lys Asp Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg
290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385 390 395

a' cont.

<210> 14
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<400> 14
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aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120

attcatgaac ccaagggcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180

agcctagaca ctcagtacac aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt 240

cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg 300

gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct 360

<210> 15
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion oligopeptide

<220>
<221> peptide
<222> (12)..(19)
<223> FLAG tag

<400> 15

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Asp Tyr Lys Asp Asp
1 5 10 15

Asp Asp Lys Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

A' Cont.

<210> 16
<211> 1612
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<213> Artificial Sequence

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<223> Fusion oligonucleotide

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<221> CDS
<222> (348)..(1559)
<223>

<220>
<221> 5'UTR
<222> (1)..(347)
<223>

<220>
<221> 3'UTR
<222> (1560)..(1612)
<223>

<220>
<221> misc_feature
<222> (1182)..(1196)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (1197)..(1220)
<223> Encodes FLAG epitope tag

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<221> misc_feature
<222> (1182)..(1159)
<223> Encodes ature fusion protein

<220>
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<222> (1182)..(1159)
<223> Encodes mature fusion protein

a' cont.

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agagcgctca tctcgatttt taccctggtg gtatactgag acaccttggt gtcagagcct     180

caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct     240

ttccttggga gaccccaccc cacaagccct gcaggggcgg ggcctccgca tcccaccttt     300

gccgagggtt cccgctctcc gaagtgccgt ggggcgccgc ctccccc atg ccg ccc       356
                                                    Met Pro Pro
                                                    1

tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta       404
Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu
    5                  10                  15

gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc       452
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Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr
20                  25                  30                  35

atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc      500
Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
                40                  45                  50

cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag      548
Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
            55                  60                  65

gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc      596
Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
        70                  75                  80

acc cgc gac cgg gtg gca ggc gag agc gcc gac cca gag ccg gag ccc      644
Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro
    85                  90                  95

gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac      692
Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp
100                 105                 110                 115

cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata      740
Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile
                120                 125                 130

tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc      788
Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro
            135                 140                 145

cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt      836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser
        150                 155                 160

gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg      884
Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
    165                 170                 175

cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg      932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp
180                 185                 190                 195

ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga      980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly
                200                 205                 210

gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc     1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser
            215                 220                 225

aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt     1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg
        230                 235                 240

cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc     1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu
    245                 250                 255

ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg     1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg
```

a' cont.

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260                 265                 270                 275

cac cgg aga gcc ctg gat acc aac gac tac aag gat gac gac gac aag     1220
His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp Asp Asp Lys
                280                 285                 290

gcc ctg gat acc aac tat tgc ttc agc tcc aca gag aag aac tgc tgt     1268
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
            295                 300                 305

gtg cgg cag ctg tac att gac ttt agg aag gac ctg ggt tgg aag tgg     1316
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
        310                 315                 320

atc cac gag ccc aag ggc tac cat gcc aac ttc tgt ctg gga ccc tgc     1364
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
    325                 330                 335

ccc tat att tgg agc ctg gac aca cag tac agc aag gtc ctt gcc ctc     1412
Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
340                 345                 350                 355

tac aac caa cac aac ccg ggc gct tcg gcg tca ccg tgc tgc gtg ccg     1460
Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys Cys Val Pro
                360                 365                 370

cag gct ttg gag cca ctg ccc atc gtc tac tac gtg ggt cgc aag ccc     1508
Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
            375                 380                 385

aag gtg gag cag ttg tcc aac atg att gtg cgc tcc tgc aag tgc agc     1556
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
        390                 395                 400

tga agccccgccc cgccccgccc ctcccggcag gcccggcccc gcccccgccc cgc      1612
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<210> 17
<211> 403
<212> PRT
<213> Artificial Sequence

a' Cont.

<220>
<223> Fusion oligonucleotide

<220>
<221> misc_feature
<222> (1182)..(1196)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (1197)..(1220)
<223> Encodes FLAG epitope tag

<220>
<221> misc_feature
<222> (1182)..(1159)
<223> Encodes ature fusion protein

<220>

<221> misc_feature
<222> (1182)..(1159)
<223> Encodes mature fusion protein

<400> 17

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Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
1               5                  10                  15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
            20                  25                  30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50                  55                  60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65                  70                  75                  80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
                85                  90                  95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
            100                 105                 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
        115                 120                 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
    130                 135                 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145                 150                 155                 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
                165                 170                 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
            180                 185                 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
        195                 200                 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
    210                 215                 220
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a' cont.

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

a' Cont.

Lys Cys Ser

<210> 18
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gccctggata ccaacgacta caaggatgac gacgacaagg ccctggatac caactactgc 60

ttcagctcca cgg 73

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
cttgtcgtcg tcatccttgt agtcgttatc cagggctcgg cggtggtgcc gggagctgtg 60

caggtgctgg gc 72

<210> 20
<211> 1624
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
<221> CDS
<222> (348)..(1571)
<223>

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<221> 5'UTR
<222> (1)..(347)
<223>

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<222> (1572)..(1624)
<223>

a' cont.

<220>
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<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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<222> (1197)..(1232)
<223> Encodes HA epitope tag

<220>
<221> misc_feature
<222> (1182)..(1571)
<223> Encodes mature fusion protein

<400> 20

ccccagcctg cctcttgagt ccctcgcatc ccaggaccct ctctcccccg agaggcagat 60

ctccctcgga cctgctggca gtagctcccc tatttaagaa cacccacttt tggatctcag 120

agagcgctca tctcgatttt taccctggtg gtatactgag acaccttggt gtcagagcct 180

caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240

ttccttggga gaccccaccc cacaagccct gcaggggcgg ggcctccgca tcccaccttt 300

gccgagggtt cccgctctcc gaagtgccgt ggggcgccgc ctccccc atg ccg ccc 356
Met Pro Pro
1

tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta 404
Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu
5 10 15

gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc 452
Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr
20 25 30 35

atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc 500
Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
40 45 50

cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag 548
Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
55 60 65

gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc 596
Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
70 75 80

acc cgc gac cgg gtg gca ggc gag agc gcc gac cca gag ccg gag ccc 644
Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro
85 90 95

gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac 692
Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp
100 105 110 115

a' cont.

cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata 740
Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile
120 125 130

tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc 788
Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro
135 140 145

cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt 836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser
150 155 160

gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg 884
Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
165 170 175

cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg 932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp
180 185 190 195

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ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga      980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly
                200                 205                 210

gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc     1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser
            215                 220                 225

aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt     1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg
        230                 235                 240

cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc     1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu
    245                 250                 255

ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg     1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg
260                 265                 270                 275

cac cgg aga gcc ctg gat acc aac agc tac cca tac gac gtg cca gac     1220
His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp Val Pro Asp
                280                 285                 290

tac gca tct ctg gcc ctg gat acc aac tat tgc ttc agc tcc aca gag     1268
Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu
            295                 300                 305

aag aac tgc tgt gtg cgg cag ctg tac att gac ttt agg aag gac ctg     1316
Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu
        310                 315                 320

ggt tgg aag tgg atc cac gag ccc aag ggc tac cat gcc aac ttc tgt     1364
Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys
    325                 330                 335

ctg gga ccc tgc ccc tat att tgg agc ctg gac aca cag tac agc aag     1412
Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys
340                 345                 350                 355

gtc ctt gcc ctc tac aac caa cac aac ccg ggc gct tcg gcg tca ccg     1460
Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro
                360                 365                 370

tgc tgc gtg ccg cag gct ttg gag cca ctg ccc atc gtc tac tac gtg     1508
Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val
            375                 380                 385

ggt cgc aag ccc aag gtg gag cag ttg tcc aac atg att gtg cgc tcc     1556
Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser
        390                 395                 400

tgc aag tgc agc tga agccccgccc cgccccgccc ctcccggcag gcccggcccc     1611
Cys Lys Cys Ser
    405

gcccccgccc cgc                                                     1624
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a' cont.

<210> 21

<211> 407
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1182)..(1196)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (1197)..(1232)
<223> Encodes HA epitope tag

<220>
<221> misc_feature
<222> (1182)..(1571)
<223> Encodes mature fusion protein

<400> 21

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

a' cont

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu

145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

a' cont.

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405

<210> 22
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gccctggata ccaacagcta cccatacgac gtgccagact acgcatctct ggccctggat 60

accaactact gcttcagctc cacggagaag aactgctgcg tgcggcag 108

<210> 23
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
cagagatgcg tagtctggca cgtcgtatgg gtagctgttg gtatccaggg ctcggcggtg 60

ccgggagctg tgc 73

<210> 24
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

a' cont.

<220>
<221> CDS
<222> (1)..(1284)
<223>

<220>
<221> misc_feature
<222> (907)..(921)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
<221> misc_feature
<222> (922)..(945)
<223> Encodes FLAG epitope tag

<220>

<221> misc_feature
<222> (907)..(1284)
<223> Encodes mature fusion protein

<400> 24

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atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg gtc ccg       48
Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1               5                   10                  15

gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat cag ttt       96
Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
            20                  25                  30

atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc aag ctg      144
Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
        35                  40                  45

aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag gtc ccc      192
Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
    50                  55                  60

ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg cag gag      240
Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65                  70                  75                  80

aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc gag cag      288
Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
                85                  90                  95

gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc cac ctc      336
Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
            100                 105                 110

ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac ttc aga      384
Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
        115                 120                 125

atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg aat ctg      432
Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
    130                 135                 140

gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa gcc aga      480
Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145                 150                 155                 160

gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc aaa gac      528
Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
                165                 170                 175

tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg aaa acc      576
Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
            180                 185                 190

aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct gtg cag      624
Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
        195                 200                 205

gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata agt tta      672
Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
    210                 215                 220
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a cont

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cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc atc ccg      720
His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225                 230                 235                 240

aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat ggc acc      768
Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
                245                 250                 255

tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act agg aaa      816
Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
            260                 265                 270

aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg ccc tcc      864
Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
        275                 280                 285

tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc gct ttg      912
Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
    290                 295                 300

gat gct gcc gac tac aag gat gac gac gac aag gct ttg gat gct gcc      960
Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala
305                 310                 315                 320

tac tgc ttt aga aat gtg cag gat aat tgc tgc ctt cgc cct ctt tac     1008
Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr
                325                 330                 335

att gat ttt aag agg gat ctt gga tgg aaa tgg atc cat gaa ccc aaa     1056
Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
            340                 345                 350

ggg tac aat gct aac ttc tgt gct ggg gca tgc cca tat cta tgg agt     1104
Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser
        355                 360                 365

tca gac act caa cac acc aaa gtc ctc agc ctg tac aac acc ata aat     1152
Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn
    370                 375                 380

ccc gaa gct tcc gct tcc cct tgc tgt gtg tcc cag gat ctg gaa cca     1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro
385                 390                 395                 400

ctg acc att ctc tat tac att gga aat acg ccc aag atc gaa cag ctt     1248
Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu
                405                 410                 415

tcc aat atg att gtc aag tct tgt aaa tgc agc taa                     1284
Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
            420                 425
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a' cont.

<210> 25
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
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<222> (907)..(921)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
<221> misc_feature
<222> (922)..(945)
<223> Encodes FLAG epitope tag

<220>
<221> misc_feature
<222> (907)..(1284)
<223> Encodes mature fusion protein

<400> 25

Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

a' cont

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala
305 310 315 320

Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
340 345 350

Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser
355 360 365

Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro
385 390 395 400

Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu
405 410 415

Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425

<210> 26
<211> 1303
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
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<222> (8)..(1303)
<223>

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<221> 5'UTR
<222> (1)..(7)
<223>

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<222> (914)..(928)
<223> Encodes amino acid residues 1-5 of TGF-beta2

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<222> (929)..(964)
<223> Encodes HA epitope tag

<220>
<221> misc_feature
<222> (914)..(1303)
<223> Encodes mature fusion protein

a' cont.

<400> 26
taaaaac atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg 49
Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu
1 5 10

gtc ccg gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat 97
Val Pro Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp
15 20 25 30

cag ttt atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc 145
Gln Phe Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser
35 40 45

aag ctg aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag 193
Lys Leu Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu
50 55 60

gtc ccc ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg 241
Val Pro Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu

```
        65                  70                  75

cag gag aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc      289
Gln Glu Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser
    80                  85                  90

gag cag gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc      337
Glu Gln Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser
95                  100                 105                 110

cac ctc ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac      385
His Leu Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr
                115                 120                 125

ttc aga atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg      433
Phe Arg Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser
            130                 135                 140

aat ctg gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa      481
Asn Leu Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys
        145                 150                 155

gcc aga gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc      529
Ala Arg Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser
    160                 165                 170

aaa gac tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg      577
Lys Asp Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val
175                 180                 185                 190

aaa acc aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct      625
Lys Thr Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala
                195                 200                 205

gtg cag gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata      673
Val Gln Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile
            210                 215                 220

agt tta cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc      721
Ser Leu His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile
        225                 230                 235

atc ccg aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat      769
Ile Pro Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp
    240                 245                 250

ggc acc tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act      817
Gly Thr Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr
255                 260                 265                 270

agg aaa aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg      865
Arg Lys Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu
                275                 280                 285

ccc tcc tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc      913
Pro Ser Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg
            290                 295                 300

gct ttg gat gct gcc agc tac cca tac gac gtg cca gac tac gca tct      961
Ala Leu Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
        305                 310                 315
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a' cont

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ctg gct ttg gat gct gcc tac tgc ttt aga aat gtg cag gat aat tgc     1009
Leu Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys
    320                 325                 330

tgc ctt cgc cct ctt tac att gat ttt aag agg gat ctt gga tgg aaa     1057
Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys
335                 340                 345                 350

tgg atc cat gaa ccc aaa ggg tac aat gct aac ttc tgt gct ggg gca     1105
Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala
                355                 360                 365

tgc cca tat cta tgg agt tca gac act caa cac acc aaa gtc ctc agc     1153
Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser
            370                 375                 380

ctg tac aac acc ata aat ccc gaa gct tcc gct tcc cct tgc tgt gtg     1201
Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val
        385                 390                 395

tcc cag gat ctg gaa cca ctg acc att ctc tat tac att gga aat acg     1249
Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr
    400                 405                 410

ccc aag atc gaa cag ctt tcc aat atg att gtc aag tct tgt aaa tgc     1297
Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys
415                 420                 425                 430

agc taa                                                            1303
Ser
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<210> 27
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

a1 cont

<220>
<221> misc_feature
<222> (914)..(928)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
<221> misc_feature
<222> (929)..(964)
<223> Encodes HA epitope tag

<220>
<221> misc_feature
<222> (914)..(1303)
<223> Encodes mature fusion protein

<400> 27

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Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1               5                   10                  15
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Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

a' cont

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala
305 310 315 320

Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu
325 330 335

Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile
340 345 350

His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro
355 360 365

Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr
370 375 380

Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln
385 390 395 400

Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys
405 410 415

a1 cont

Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425 430

<210> 28
<211> 1272
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
<221> CDS
<222> (1)..(1272)
<223>

<220>
<221> misc_feature

<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (910)..(933)
<223> Encodes FLAG epitope tag

<220>
<221> misc_feature
<222> (895)..(1272)
<223> Encodes mature fusion protein

<400> 28

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atg cac ttg caa agg gct ctg gta gtc ctg gcc ctg ctg aac ttg gcc       48
Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1               5                   10                  15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac       96
Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
            20                  25                  30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag      144
Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
        35                  40                  45

ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc      192
Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
    50                  55                  60

tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag      240
Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65                  70                  75                  80

atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct      288
Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
                85                  90                  95

gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg      336
Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
            100                 105                 110

gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag      384
Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
        115                 120                 125

gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg      432
Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
    130                 135                 140

ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag      480
Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145                 150                 155                 160

cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag      528
Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
                165                 170                 175
```

a' cont

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cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg      576
His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
            180                 185                 190

ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag      624
Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
        195                 200                 205

tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac      672
Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
    210                 215                 220

tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt      720
Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225                 230                 235                 240

cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac      768
His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
                245                 250                 255

cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac      816
His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
            260                 265                 270

aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc      864
Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
        275                 280                 285

cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat gac      912
Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
    290                 295                 300

tac aag gat gac gac gac aag gcc ctg gac acc aat tac tgc ttc cgc      960
Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
305                 310                 315                 320

aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat att gac ttc cgg     1008
Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
                325                 330                 335

cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag ggt tac tat gcc     1056
Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
            340                 345                 350

aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc gca gac aca acc     1104
Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
        355                 360                 365

cat agc acg gtg ctt gga cta tac aac acc ctg aac cca gag gcg tct     1152
His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser
    370                 375                 380

gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc ctg acc atc ttg     1200
Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
385                 390                 395                 400

tac tat gtg ggc aga acc ccc aag gtg gag cag ctg tcc aac atg gtg     1248
Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val
                405                 410                 415

gtg aag tcg tgt aag tgc agc tga                                    1272
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a' cont

Val Lys Ser Cys Lys Cys Ser
420

<210> 29
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
<221> misc_feature
<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (910)..(933)
<223> Encodes FLAG epitope tag

<220>
<221> misc_feature
<222> (895)..(1272)
<223> Encodes mature fusion protein

<400> 29

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

a' cont.

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
290 295 300

a' cont

Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
305 310 315 320

Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
325 330 335

Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
340 345 350

Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
355 360 365

His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser

370 375 380

Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
385 390 395 400

Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val
405 410 415

Val Lys Ser Cys Lys Cys Ser
420

<210> 30
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
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<222> (1)..(1284)
<223>

<220>
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<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (910)..(945)
<223> Encodes HA epitope tag

a1 Cont.

<220>
<221> misc_feature
<222> (895)..(1284)
<223> Encodes mature fusion protein

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Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192

```
Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
    50                  55                  60

tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag      240
Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65                  70                  75                  80

atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct      288
Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
                85                  90                  95

gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg      336
Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
            100                 105                 110

gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag      384
Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
        115                 120                 125

gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg      432
Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
    130                 135                 140

ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag      480
Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145                 150                 155                 160

cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag      528
Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
                165                 170                 175

cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg      576
His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
            180                 185                 190

ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag      624
Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
        195                 200                 205

tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac      672
Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
    210                 215                 220

tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt      720
Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225                 230                 235                 240

cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac      768
His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
                245                 250                 255

cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac      816
His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
            260                 265                 270

aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc      864
Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
        275                 280                 285

cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat agc      912
Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
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a' cont.

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    290                 295                 300

tac cca tac gac gtg cca gac tac gca tct ctg gcc ctg gac acc aat      960
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
305                 310                 315                 320

tac tgc ttc cgc aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat     1008
Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
                325                 330                 335

att gac ttc cgg cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag     1056
Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
            340                 345                 350

ggt tac tat gcc aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc     1104
Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
        355                 360                 365

gca gac aca acc cat agc acg gtg ctt gga cta tac aac acc ctg aac     1152
Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
    370                 375                 380

cca gag gcg tct gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc     1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
385                 390                 395                 400

ctg acc atc ttg tac tat gtg ggc aga acc ccc aag gtg gag cag ctg     1248
Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
                405                 410                 415

tcc aac atg gtg gtg aag tcg tgt aag tgc agc tga                     1284
Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
            420                 425
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<210> 31
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

a' Cont.

<220>
<221> misc_feature
<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (910)..(945)
<223> Encodes HA epitope tag

<220>
<221> misc_feature
<222> (895)..(1284)
<223> Encodes mature fusion protein

<400> 31

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala

1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

A' cont.

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
290 295 300

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
305 310 315 320

Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
340 345 350

Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
355 360 365

Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
385 390 395 400

Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
405 410 415

a' Cont.

Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
420 425

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           Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
           1               5                  10

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga        97
Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
    15                  20                  25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc       145
Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
30                  35                  40                  45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc       193
Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
                50                  55                  60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta       241
Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
            65                  70                  75

ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc       289
Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
        80                  85                  90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc       337
Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
    95                  100                 105

cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag       385
Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
110                 115                 120                 125
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a' cont.

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ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg      433
Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg
                130                 135                 140

gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg      481
Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu
            145                 150                 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa      529
Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys
        160                 165                 170

tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc      577
Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro
    175                 180                 185

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg      625
Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
190                 195                 200                 205

cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc      673
Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala
                210                 215                 220

cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac      721
His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn
            225                 230                 235

ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg      769
Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met
        240                 245                 250

aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag      817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
    255                 260                 265

cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac tac      865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr
270                 275                 280                 285

aag gat gac gac gac aag gcc ctg gat acc aac tac tgc ttc agc tcc      913
Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
                290                 295                 300

acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg aag      961
Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
            305                 310                 315

gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc aat     1009
Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
        320                 325                 330

ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag tac     1057
Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
    335                 340                 345

agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg gcg     1105
Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
350                 355                 360                 365
```

A1 cont.

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gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg tac     1153
Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
                370                 375                 380

tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc gtg     1201
Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
            385                 390                 395

cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc cccgcccacc        1252
Arg Ser Cys Lys Cys Ser
        400

cggcaggccc ggccccaccc ccgcccgcct caccggggct gtatttaagg acatcgtgcc   1312

ccaagcccac ttgggatcga ttaaagcggc cgcgact                            1349
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<223> Encodes amino acid residues 1-5 of TGF-beta1

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a' cont.

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
            20                  25                  30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50                  55                  60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65                  70                  75                  80
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Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

a1 cont. Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

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                1               5                   10

ctg ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc        98
Leu Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala
        15                  20                  25

gga ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag       146
Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys
    30                  35                  40

cgc atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc       194
Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala
45                  50                  55                  60

agc ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca       242
Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala
                65                  70                  75

gta ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt       290
Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser
            80                  85                  90

gtc gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc       338
Val Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val
        95                  100                 105

acc cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc       386
Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe
    110                 115                 120

aag ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc       434
Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu
125                 130                 135                 140

cgg gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc       482
Arg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg
                145                 150                 155

ctg ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag       530
Leu Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln
            160                 165                 170

aaa tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc       578
Lys Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala
        175                 180                 185
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a' cont.

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ccc agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg      626
Pro Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val
    190                 195                 200

cgg cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt      674
Arg Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser
205                 210                 215                 220

gcc cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att      722
Ala His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile
                225                 230                 235

aac ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc      770
Asn Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly
            240                 245                 250

atg aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc      818
Met Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala
        255                 260                 265

cag cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac      866
Gln His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp
    270                 275                 280

tac aag gat gac gac gac aag gcc ctg gat acc aac tac tgc ttc agc      914
Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser
285                 290                 295                 300

tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg      962
Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
                305                 310                 315

aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc     1010
Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
            320                 325                 330

aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag     1058
Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
        335                 340                 345

tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg     1106
Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
    350                 355                 360

gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg     1154
Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
365                 370                 375                 380

tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc     1202
Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
                385                 390                 395

gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc cccgcccacc    1256
Val Arg Ser Cys Lys Cys Ser
            400

cggcaggccc ggccccaccc ccgcccgcct caccggggct gtatttaagg acatcgtgcc   1316

ccaagcccac ttgggatcga ttaaagcggc cgcgact                            1353
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<223> Encodes mature fusion protein

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

a' Cont.

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

```
His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
    130                 135                 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145                 150                 155                 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
                165                 170                 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
            180                 185                 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
        195                 200                 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
    210                 215                 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225                 230                 235                 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
                245                 250                 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
            260                 265                 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
        275                 280                 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
    290                 295                 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305                 310                 315                 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
                325                 330                 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
            340                 345                 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
        355                 360                 365
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a' cont.

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

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a1 cont

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
1 5 10

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ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga        97
Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
    15                  20                  25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc       145
Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
30                  35                  40                  45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc       193
Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
                50                  55                  60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta       241
Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
            65                  70                  75

ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc       289
Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
        80                  85                  90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc       337
Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
    95                  100                 105

cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag       385
Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
110                 115                 120                 125

ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg       433
Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg
                130                 135                 140

gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg       481
Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu
            145                 150                 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa       529
Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys
        160                 165                 170

tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc       577
Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro
    175                 180                 185

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg       625
Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
190                 195                 200                 205

cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc       673
Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala
                210                 215                 220

cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac       721
His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn
            225                 230                 235

ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg       769
Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met
        240                 245                 250
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a1 cont

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aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag      817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
    255                 260                 265

cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac      865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr
270                 275                 280                 285

cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac      913
Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr
                290                 295                 300

tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att      961
Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile
            305                 310                 315

gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc     1009
Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly
        320                 325                 330

tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta     1057
Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu
    335                 340                 345

gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg     1105
Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro
350                 355                 360                 365

ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg     1153
Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu
                370                 375                 380

ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc     1201
Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser
            385                 390                 395

aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc   1254
Asn Met Ile Val Arg Ser Cys Lys Cys Ser
        400                 405

cccgcccacc cggcaggccc ggccccaccc ccgcccgcct caccggggct gtatttaagg   1314

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<223> Encodes HA epitope tag

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

a' cont

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
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<223> Encodes mature fusion protein

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tggtaccgag atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg        49
           Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
           1               5                   10

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga        97
Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
    15                  20                  25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc       145
Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
30                  35                  40                  45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc       193
Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
                50                  55                  60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta       241
Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
            65                  70                  75

ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc       289
Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
        80                  85                  90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc       337
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a' cont

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Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
    95                  100                 105

cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag      385
Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
110                 115                 120                 125

ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg      433
Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg
                130                 135                 140

gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg      481
Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu
            145                 150                 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa      529
Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys
        160                 165                 170

tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc      577
Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro
    175                 180                 185

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg      625
Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
190                 195                 200                 205

cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc      673
Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala
                210                 215                 220

cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att aac      721
His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn
            225                 230                 235

ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg      769
Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met
        240                 245                 250

aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag      817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
    255                 260                 265

cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac      865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr
270                 275                 280                 285

cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac      913
Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr
                290                 295                 300

tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att      961
Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile
            305                 310                 315

gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc     1009
Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly
        320                 325                 330

tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta     1057
Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu
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a1 cont

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    335                 340                 345

gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg     1105
Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro
350                 355                 360                 365

ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg     1153
Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu
                370                 375                 380

ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc     1201
Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser
            385                 390                 395

aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc   1254
Asn Met Ile Val Arg Ser Cys Lys Cys Ser
        400                 405

cccgcccacc cggcaggccc ggccccaccc ccgcccgcct caccggggct gtatttaagg   1314

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<220>
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<220>
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<400>  39

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1               5                   10                  15


Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
            20                  25                  30


Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45


Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
```

a' cont

50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

A1 Cont

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

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Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305                 310                 315                 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
                325                 330                 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
            340                 345                 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
        355                 360                 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
    370                 375                 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385                 390                 395                 400

Val Arg Ser Cys Lys Cys Ser
                405
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a' cont